SEQUENCE LISTING

<110> WINDSOR-HINES, Dawn RAO, Patricia RINGLER, Douglas J. <120> INDUCING TOLERANCE IN PRIMATES <130> TLN-022 <150> 60/431839 <151> 2002-12-09 <160>70 <170> FastSEQ for Windows Version 4.0 <210>1 <211>717 <212> DNA <213> Artificial Sequence <220> <223> Chimeric Sequence <221> CDS <222>(1)...(717) atg gag aca gac aca atc ctg cta tgg gtg ctg ctg ctc tgg gtt cca 48 Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro 10 ggc tcc act ggt gac att gtg atg acc caa tct cca gat tct ttg gct 96 Gly Ser Thr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala . 20 25 30 gtg tct cta ggt gag agg gcc acc atc aac tgc aag gcc agc caa agt 144 Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser 40 35 45 gtt gat tat gat ggt gat agt tat atg aac tgg tat caa cag aaa cca 192 Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro 50 55 gga cag cca ccc aaa ctc ctc atc tat gtt gca tcc aat cta gag tct 240 Gly Gln Pro Pro Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser 65 70 75 ggg gtc cca gac agg ttt agt ggc agt ggg tct ggg aca gac ttc acc 288 Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr 90 95 85

ctc acc atc agt tct ctg cag gcg gag gat gtt gca gtc tat tac tgt 336 Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys

100 105 110

cag caa agt ctt cag gac cct ccg acg ttc ggt gga ggt acc aag gtg 384 Gln Gln Ser Leu Gln Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val 115 120 125

gaa atc aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca 432 Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro 130 135 140

tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg 480 Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu 145 150 155 160

aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac 528 Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn 165 170 175

gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc 576 Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser 180 185 190

aag gac agc acc tac agc ctc agc agc acc ctg agc aaa gca 624 Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala 195 200 205

gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc 672 Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly 210 215 220

ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag
717
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225
230
235

<210>2

<211>716

<212> DNA

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400> 2

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<210>4 <211>218 <212> PRT <213> Artificial Sequence

<220>

<223> Chimeric Sequence Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly

10 Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp 20 25 30

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                 40
                              45
Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser Gly Val Pro Asp
  50
               55
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
             70
                         75
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Ser Leu
                      90
                                   95
Gln Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
                    105
                                  110
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
                  120
                                125
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
  130
                             140
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
             150
                           155
                                         160
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
                       170
                                     175
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
                                  190
                    185
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
    195
                  200
                               205
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
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               215
<210>5
<211> 1404
<212> DNA
<213> Artificial Sequence
<223> Chimeric Sequence
<221> CDS
<222> (1)...(1404)
<400> 5
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Met Glu Trp Ile Trp Ile Phe Leu Leu Ile Leu Ser Gly Thr Arg Gly
                       10
                                    15
gtc cag tcc cag gtt cag ctg gtg cag tct gga gct gaa gtg aag aag 96
Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
       20
                    25
cct ggg gct tca gtg aag gtg tcc tgt aag gct tct gga tac aca ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
     35
                  40
                               45
act gcc tat gtt ata agc tgg gtg agg cag gca cct gga cag ggc ctt 192
Thr Ala Tyr Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
               55
gag tgg atg gga gag att tat cct gga agc ggt agt agt tat tat aat 240
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Glu Trp Met Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn

65 70 75 80 gag aag ttc aag ggc agg gtc aca atg act aga gac aca tcc acc agc 288 Glu Lys Phe Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser 85 90 aca gtc tac atg gaa ctc agc agc ctg agg tct gag gac act gcg gtc 336 Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val 100 105 110 tat tac tgt gca aga tcc ggg gac ggc agt cgg ttt gtt tac tgg ggc 384 Tyr Tyr Cys Ala Arg Ser Gly Asp Gly Ser Arg Phe Val Tyr Trp Gly 115 120 125 caa ggg aca cta gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg 432 Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser 130 135 140 gte tte eec etg gea eec tee tee aag age ace tet ggg gge aca geg 480 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala 145 150 155 160 gec etg gge tge etg gte aag gae tae tte eee gaa eeg gtg aeg gtg 528 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val 170 165 175 teg tgg aac tea gge gee etg ace age gge gtg cae ace tte eeg get 576 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala 180 185 gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg 624 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val 200 ccc tcc age age ttg ggc acc cag acc tac atc tgc aac gtg aat cac 672 Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His 210 215 220 aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt 720 Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys 225 230 235 gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc gcg ggg 768 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Ala Gly 245 250 255 gea eeg tea gte tte ete tte eec eea aaa eec aag gae ace ete atg 816 Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met 260 265 270 atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac 864

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg 912 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val

285

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

280

275

290 295 300

cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac 960 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr 305 310 315 320

cgt gtg gtc agc gtc ctc 'acc gtc ctg cac cag gac tgg ctg aat ggc 1008 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly 325 330 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc 1056 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile 340 345 350

gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg 1104 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val 355 360 365

tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc 1152 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser 370 375 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag 1200 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu 385 390 395 400

tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc 1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg 1296 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val 420 425 430

gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg 1344 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met 435 440 445

cat gag get etg cae aac cae tae aeg cag aag age ete tee etg tet 1392 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser 450 455 460

ccg ggt aaa tga Pro Gly Lys * 465 1404

<210>6

<211> 1404

<212> DNA

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400> 6

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<210>7
<211>467
<212> PRT
<213> Artificial Sequence
<220>
<223> Chimeric Sequence
<400> 7
Met Glu Trp Ile Trp Ile Phe Leu Leu Ile Leu Ser Gly Thr Arg Gly
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                      10
Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
                                30
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
                              45
Thr Ala Tyr Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
                           60
Glu Trp Met Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn
            70
                         75
                                      80
Glu Lys Phe Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
                     90
                                   95
Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
                    105
                                  110
Tyr Tyr Cys Ala Arg Ser Gly Asp Gly Ser Arg Phe Val Tyr Trp Gly
                  120
                               125
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
  130
               135
                             140
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
             150
                          155
                                        160
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
         165
                      170
                                    175
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Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His 210 215 220
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys 225 230 235 240
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Ala Gly
Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly 325 330 335
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile 340 345 350
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val 355 360 365
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser 370 375 380
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met 435 440 445
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser 450 455 460
Pro Gly Lys
465
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<211> 448
<212> PRT <213> Artificial Sequence
<220>
<223> Chimeric Sequence
<400> 8
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala 1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ala Tyr 20 25 30
Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45 Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn Glu Lys Phe

50 55 60	
Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr	
65 70 75 80	
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95	
Ala Arg Ser Gly Asp Gly Ser Arg Phe Val Tyr Trp Gly Gln Gly Thr 100 105 110	
Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro 115 120 125	
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly 130 135 140	
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn	
145 150 155 160	
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln 165 170 175	
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser	
180 185 190	
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser 195 200 205	
Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys The 210 215 220	r
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Ala Gly Ala Pro Ser 225 230 235 240	
$\label{thm:continuous} \textbf{Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg}$	
245 250 255 Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro 260 265 270	
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala 275 280 285	ì
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val	
290 295 300 Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr	r
305 310 315 320	
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr 325 330 335	
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu 340 345 350	
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys 355 360 365	
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser 370 375 380	
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp	p
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser	
405 410 415 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala 420 425 430	
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys 435 440 445	
130 170 170	

<210>9

<211>717

<212> DNA <213> Artificial Sequence

<220> <223> Chimeric Sequence
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ggc tcc act ggt gac att gtg atg acc caa tct cca gat tct ttg gct 96 Gly Ser Thr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala 20 25 30
gtg tct cta ggt gag agg gcc acc atc aac tgc aag gcc agc caa agt 144 Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser 35 40 45
gtt gat tat gat ggt gat agt tat atg aac tgg tat caa cag aaa cca 192 Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro 50 55 60
gga cag cca ccc aaa ctc ctc atc tat gtt gca tcc aat cta gag tct 240 Gly Gln Pro Pro Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser 65 70 75 80
ggg gtc cca gac agg ttt agt ggc agt ggg tct ggg aca gac ttc acc 288 Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr 85 90 95
ctc acc atc agt tct ctg cag gcg gag gat gtt gca gtc tat tac tgt 336 Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys 100 105 110
cag caa agt ctt cag gac cct ccg acg ttc ggt gga ggt acc aag gtg 384 Gln Gln Ser Leu Gln Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val 115 120 125
gaa atc aaa cga act gtg gct gca cta tct gtc ttc atc ttc ccg cca 432 Glu Ile Lys Arg Thr Val Ala Ala Leu Ser Val Phe Ile Phe Pro Pro 130 135 140
tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg 480 Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu 145 150 155 160
aat aac tte tat eec aga gag gee aaa gta eag tgg aag gtg gat aac 528 Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn 165 170 175
gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc 576 Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser 180 185 190
aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca 624

Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala 195 200 205

gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc 672 Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly 210 215 220

ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gga tgt tag

717
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

225
230
235

<210> 10

<211>717

<212> DNA

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400> 10

atggagacag acacaatcct gctatgggtg ctgctgctct gggttccagg ctccactggt 60 gacattgtga tgacccaatc tccagattct ttggctgtgt ctctaggtga gagggccacc 120 atcaactgca aggccagcca aagtgttgat tatgatggtg atagttatat gaactggtat 180 caacagaaac caggacagcc acccaaactc ctcatctatg ttgcatccaa tctagagtct 240 ggggtcccag acaggtttag tggcagtggg tctgggacag acttcaccct caccatcagt 300 tctctgcagg cggaggatgt tgcagtcat tactgtcagc aaagtcttca ggaccctccg 360 acgttcggtg gaggtaccaa ggtggaaatc aaacgaactg tggctgcact atctgtcttc 420 atcttcccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg 480 aataacttct atcccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg 540 ggtaactccc aggagaggtg cacagagcag gacagcaagg acagcacta cagcctcagc 600 agcaccctga cgctgagcaa agcagcatca gagaaacaca aagtctacgc ctgcgaagtc 660 acccatcagg gcctgagctc gcccgtcaca aagagcttca acaggggaga gtgttag 717

<210> 11

<211>238

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400> 11

Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro 1 5 10 15

Gly Ser Thr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala 20 25 30

Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser 35 40 45

Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro 50 55 60

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser 65 70 75 80

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr 85 90 95

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Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
                    105
                                 110
Gln Gln Ser Leu Gln Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
     115
                  120
                               125
Glu Ile Lys Arg Thr Val Ala Ala Leu Ser Val Phe Ile Phe Pro Pro
               135
                            140
Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
             150
                          155
                                        160
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
                      170
         165
                                    175
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
       180
                    185
                                 190
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
                  200
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
                            220
               215
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
             230
                          235
<210> 12
<211>218
<212> PRT
<213> Artificial Sequence
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<223> Chimeric Sequence
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Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
                      10
Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
       20
                   25
                                30
Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
    35
                 40
                              45
Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser Gly Val Pro Asp
               55
                           60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
            70
                         75
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Ser Leu
                      90
                                  95
Gln Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
       100
                    105
                                 110
Thr Val Ala Ala Leu Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
                  120
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
  130
               135
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
             150
                          155
                                        160
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
                      170
                                    175
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
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                    185
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
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                               205
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
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Tyr Tyr Cys Ala Arg Ser Gly Asp Gly Ser Arg Phe Val Tyr Trp Gly 115 125

caa ggg aca cta gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg 432 Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser 130 135 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg 480 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala 145 150 155 160

gee etg gge tge etg gte aag gae tae tte eee gaa eeg gtg aeg gtg 528

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val

tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct 576 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala 180 185 190

gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg 624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac 672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt 720 Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys 225 230 235 240

gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg 768 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly 245 250 255

gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg 816 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met 260 265 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac 864

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

275 280 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg 912 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val 290 295 300

cat aat gcc aag aca aag ccg cgg gag gag cag tac gcc agc acg tac 960 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr 305 310 315 320

cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc 1008 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly 325 330 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc 1056 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile 340 345 350

gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg 1104 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val 355 360 365

tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc 1152 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser 370 375 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag 1200

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu 385 390 395 400

tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc 1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg 1296 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val 420 425 430

gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg 1344 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met 435 440 445

cat gag get etg cac aac cac tac aeg eag aag age ete tee etg tet 1392 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser 450 455 460

ccg ggt aaa tga Pro Gly Lys * 465 1404

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<211> 1404

<212> DNA

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400> 14

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ctctccctgt ctccgggtaa atga	1404
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20 25 30 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala S 35 40 45	•
Thr Ala Tyr Val Ile Ser Trp Val Arg Gln Ala P 50 55 60	
Glu Trp Met Gly Glu Ile Tyr Pro Gly Ser Gly S 65 70 75 80 Glu Lys Phe Lys Gly Arg Val Thr Met Thr Arg	
85 90 95 Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser 100 105 110	Glu Asp Thr Ala Val
Tyr Tyr Cys Ala Arg Ser Gly Asp Gly Ser Arg 115 120 125 Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser T	
130 135 140 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr S	
145 150 155 160 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro 165 170 175	
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val I 180 185 190 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser S	
195 200 205 Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cy 210 215 220	ys Asn Val Asn His
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val 225 230 235 240	
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala 245 250 255 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro I	_
260 265 270 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val V 275 280 285	al Asp Val Ser His
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val 290 295 300 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln	
305 310 315 320 Arg Val Val Ser Val Leu Thr Val Leu His Gln	
325 330 335	Lau Dua Ala Dua Ila

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile 340 345 350 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

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355
                  360
                               365
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
  370
               375
                            380
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385
             390
                          395
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                      410
                                   415
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                    425
                                 430
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
                  440
                               445
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
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                            460
Pro Gly Lys
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ala Tyr
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Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
    35
                 40
                              45
Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn Glu Lys Phe
               55
                           60
Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65
                         75
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                      90
Ala Arg Ser Gly Asp Gly Ser Arg Phe Val Tyr Trp Gly Gln Gly Thr
                    105
                                 110
Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
                  120
                               125
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
               135
                            140
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
             150
                          155
                                        160
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                      170
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
                                 190
                    185
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
                 200
                               205
Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
               215
                            220
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225
             230
                          235
                                        240
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Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg 250 255 Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro 260 265 Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala 280 285 Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val 295 300 Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr 310 315 320 Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr 325 330 335 Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu 340 345 350 Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys 360 365 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser 375 380 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp 395 400 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser 405 410 415 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala 425 430 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys 435 440 <210> 17 <211>717 <212> DNA <213> Artificial Sequence <220> <223> Chimeric Sequence <221> CDS <222>(1)...(717) atg gag aca gac aca atc ctg cta tgg gtg ctg ctg ctc tgg gtt cca 48 Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro 5 10 ggc tcc act ggt gac att gtg atg acc caa tct cca gat tct ttg gct 96 Gly Ser Thr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala 20 25 30 gtg tct cta ggt gag agg gcc acc atc aac tgc aag gcc agc caa agt 144 Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser 35 40 45 gtt gat tat gat ggt gat agt tat atg aac tgg tat caa cag aaa cca 192 Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro 50 55

gga cag cca ccc aaa ctc ctc atc tat gtt gca tcc aat cta gag tct 240 Gly Gln Pro Pro Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser 65 70 75 80

ggg gtc cca gac agg ttt agt ggc agt ggg tct ggg aca gac ttc acc 288 Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr 85 90 95

ctc acc atc agt tct ctg cag gcg gag gat gtt gca gtc tat tac tgt 336 Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys 100 105 110

cag caa agt ctt cag gac cct ccg acg ttc ggt gga ggt acc aag gtg 384 Gln Gln Ser Leu Gln Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val 115 120 125

gaa atc aaa cga act gtg gct gca cta tct gtc ttc atc ttc ccg cca 432 Glu Ile Lys Arg Thr Val Ala Ala Leu Ser Val Phe Ile Phe Pro Pro 130 135 140

tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg 480 Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu 145 150 155 160

aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac 528 Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn 165 170 175

gcc etc caa teg ggt aac tee cag gag agt gte aca gag cag gac age 576 Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser 180 185 190

aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca 624 Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala 195 200 205

gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc 672 Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly 210 215 220

ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag
717
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
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225
230
235

<210> 18

<211>717

<212> DNA

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

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<211>238
<212> PRT
<213> Artificial Sequence
<223> Chimeric Sequence
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Gly Ser Thr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
                   25
                                30
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser
                 40
                              45
Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
               55
                           60
Gly Gln Pro Pro Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser
                         75
                                      80
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
                     90
Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
                    105
                                 110
Gln Gln Ser Leu Gln Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
    115
                  120
                               125
Glu Ile Lys Arg Thr Val Ala Ala Leu Ser Val Phe Ile Phe Pro Pro
                             140
Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
             150
                          155
                                       160
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
         165
                      170
                                   175
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
      180
                    185
                                 190
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
                 200
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
                            220
               215
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225
             230
                          235
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<212> PRT <213> Artificial Sequence <220> <223> Chimeric Sequence <400> 20 Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly 10 Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp 25 30 Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro 40 45 Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser Gly Val Pro Asp 55 60 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser 75 Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Ser Leu 90 95 Gln Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg 105 110 Thr Val Ala Ala Leu Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln 120 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr 130 140 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser 150 155 160 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr 170 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys 185 190 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro 195 200 205 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys 210 215 <210>21 <211> 1404 <212> DNA <213> Artificial Sequence <223> Chimeric Sequence <221> CDS <222> (1)...(1404) <400> 21 atg gaa tgg atc tgg atc ttt ctc ctc atc ctg tca gga act cga ggt 48 Met Glu Trp Ile Trp Ile Phe Leu Leu Ile Leu Ser Gly Thr Arg Gly 5 10 15 gtc cag tcc cag gtt cag ctg gtg cag tct gga gct gaa gtg aag aag 96

Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys

30

25

20

cct ggg gct tca gtg aag gtg tcc tgt aag gct tct gga tac aca ttc 144 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe 35 40 45

act gcc tat gtt ata agc tgg gtg agg cag gca cct gga cag ggc ctt 192 Thr Ala Tyr Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu 50 55 60

gag tgg atg gga gag att tat cct gga agc ggt agt agt tat tat aat 240 Glu Trp Met Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn 65 70 75 80

gag aag ttc aag ggc agg gtc aca atg act aga gac aca tcc acc agc 288 Glu Lys Phe Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser 85 90 95

aca gtc tac atg gaa ctc agc agc ctg agg tct gag gac act gcg gtc 336
Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

tat tac tgt gca aga tcc ggg gac ggc agt cgg ttt gtt tac tgg ggc 384
Tyr Tyr Cys Ala Arg Ser Gly Asp Gly Ser Arg Phe Val Tyr Trp Gly
115 120 125

caa ggg aca cta gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg 432 Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser 130 135 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg 480 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala 145 150 155 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg 528 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val 165 170 175

tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct 576 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala 180 185 190

gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg 624 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val 195 200 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac 672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt 720 Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys 225 230 235 240

gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc gcg ggg 768 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Ala Gly 245 250 255

gca ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg 816 Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met 260 265 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gtg gtg agc cac 864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg 912 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val 290 295 300

cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac 960 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr 305 310 315 320

cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc 1008 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly 325 330 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc 1056 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile 340 345 350

gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg 1104 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val 355 360 365

tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc 1152 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser 370 375 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag 1200 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu 385 390 395 400

tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc 1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg 1296 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val 420 425 430

gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg 1344 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met 435 440 445

cat gag get etg cac aac cac tac aeg cag aag age etc tee etg tet 1392 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser 450 455 460

ccg ggt aaa tga Pro Gly Lys * 465 1404

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<400> 22

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<210> 23 <211>467 <212> PRT <213> Artificial Sequence <220> <223> Chimeric Sequence <400> 23 Met Glu Trp Ile Trp Ile Phe Leu Leu Ile Leu Ser Gly Thr Arg Gly 5 10 15 Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys 25 30 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe 40 45 Thr Ala Tyr Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu 55 60 Glu Trp Met Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn 75 Glu Lys Phe Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser

<213> Artificial Sequence

Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Gly Asp Gly Ser Arg Phe Val Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile -345 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys <210> 24 <211>448 <212> PRT

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<223> Chimeric Sequence

<400> 24

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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ala Tyr
20 25 30

Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met 35 40 45

Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn Glu Lys Phe 50 55 60

Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95

Ala Arg Ser Gly Asp Gly Ser Arg Phe Val Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro 115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly 130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn 145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln 165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser 180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser 195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr 210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Ala Gly Ala Pro Ser 225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg 245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro 260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala 275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val 290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr 305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr 325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu 340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys 355 360 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser 370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp 385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser 405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala 425 430 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys 440 435 445 <210> 25 <211>717 <212> DNA <213> Artificial Sequence <220> <223> Chimeric Sequence <221> CDS <222> (1)...(717) <400> 25 atg gag aca gac aca atc ctg cta tgg gtg ctg ctg ctc tgg gtt cca 48 Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro 5 10 1 15 ggc tcc act ggt gac att gtg atg acc caa tct cca gat tct ttg gct 96 Gly Ser Thr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala 20 25 30 gtg tet eta ggt gag agg gee ace ate aac tge aag gee age caa agt 144 Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser 35 gtt gat tat gat ggt gat agt tat atg aac tgg tat caa cag aaa cca 192 Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro gga cag cca ccc aaa ctc ctc atc tat gtt gca tcc aat cta gag tct 240 Gly Gln Pro Pro Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser 70 75 65 ggg gtc cca gac agg ttt agt ggc agt ggg tct ggg aca gac ttc acc 288 Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr 90 95 85 ctc acc atc agt tct ctg cag gcg gag gat gtt gca gtc tat tac tgt 336 Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys 100 105 110 cag caa agt ctt cag gac cct ccg acg ttc ggt gga ggt acc aag gtg 384 Gln Gln Ser Leu Gln Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val 115 120 gaa atc aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca 432

gaa atc aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca 432
Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
130 135 140

tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg 480 Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu

145

150

155

160

aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac 528 Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn 165 170 175

gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc 576 Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser 180 185 190

aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca 624 Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala 195 200 205

gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc 672 Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly 210 215 220

ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag

717

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

225

230

235

<210> 26

<211>716

<212> DNA

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400> 26

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<210>27

<211>238

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400> 27

Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro

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Gly Ser Thr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser
                 40
                              45
Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
               55
                           60
Gly Gln Pro Pro Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser
                         75
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
                     90
                                  95
Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
                    105
                                 110
Gln Gln Ser Leu Gln Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
    115
                 120
                               125
Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
                            140
               135
Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
             150
                          155
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
                      170
         165
                                   175
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
                    185
                                 190
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
                 200
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
                            220
               215
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
             230
                          235
<210>28
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<212> PRT
<213> Artificial Sequence
<223> Chimeric Sequence
<400> 28
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
                     10
Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
                   25
                                30
Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
                 40
                              45
Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser Gly Val Pro Asp
               55
Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
                         75
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Ser Leu
                     90
Gln Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
                    105
                                 110
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
    115
                  120
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Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
   130
                 135
                              140
 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
 145
               150
                            155
 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
          165
                        170
                                      175
 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
                     185
                                   190
 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                   200
 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
   210
                215
<210>29
 <211> 1404
 <212> DNA
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 <220>
 <223> Chimeric Sequence
 <221> CDS
 <222>(1)...(1404)
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 atg gaa tgg atc tgg atc ttt ctc ctc atc ctg tca gga act cga ggt 48
 Met Glu Trp Ile Trp Ile Phe Leu Leu Ile Leu Ser Gly Thr Arg Gly
           5
                        10
 gtc cag tcc cag gtt cag ctg gtg cag tct gga gct gaa gtg aag aag 96
 Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 cct ggg gct tca gtg aag gtg tcc tgt aag gct tct gga tac aca ttc 144
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
      35
                   40
                                45
 act gcc tat gtt ata agc tgg gtg agg cag gca cct gga cag ggc ctt 192
 Thr Ala Tyr Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
    50
                 55
gag tgg atg gga gag att tat cct gga agc ggt agt agt tat tat aat 240
 Glu Trp Met Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn
< 65
              70
                            75
 gag aag ttc aag ggc agg gtc aca atg act aga gac aca tcc acc agc 288
 Glu Lys Phe Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
                        90
           85
 aca gtc tac atg gaa ctc agc agc ctg agg tct gag gac act gcg gtc 336
Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
        100
                      105
                                   110
 tat tac tgt gca aga tcc ggg gac ggc agt cgg ttt gtt tac tgg ggc 384
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Tyr Tyr Cys Ala Arg Ser Gly Asp Gly Ser Arg Phe Val Tyr Trp Gly

115 120 125

caa ggg aca cta gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg 432 Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser 130 135 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg 480 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala 145 150 155 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg 528

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val

165 170 175

teg tgg aac tea gge gee etg ace age gge gtg eac ace tte eeg get 576 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala 180 185 190

gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg 624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac 672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt 720 Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys 225 230 235 240

gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg 768 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly 245 250 255

gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg 816 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met 260 265 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gtg gtg agc cac 864

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

275 280 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg 912 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val 290 295 300

cat aat gcc aag aca aag ccg cgg gag gag cag tac gcc agc acg tac 960 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr 305 310 315 320

cgt gtg gtc agc gtc ctc ace gtc ctg cac cag gac tgg ctg aat ggc 1008 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly 325 330 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc 1056 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile

340 345 350

gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg 1104 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val 355 360 365

tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc 1152 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser 370 375 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag 1200 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu 385 390 395 400

tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc 1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg 1296 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val 420 425 430

gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg 1344 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met 435 440 445

cat gag get etg cac aac cac tac aeg eag aag age etc tee etg tet 1392 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser 450 455 460

ccg ggt aaa tga Pro Gly Lys * 465 1404

<210>30

<211> 1404

<212> DNA

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400>30

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gacaaaactc acacatgccc accgtgccca gcacctgaac teetgggggg accgtcagte 780 tteetettee ecceaaaace caaggacace eteatgatet eccggacece tgaggteaa 840 tgegtggtgg tggacgtgag ceacgaagac ectgaggtea agtteaactg gtacgtggac 900 ggegtggagg tgeataatge eaagacaaag eegegggagg ageagtaege eageacgtae 960 egtgtggtea gegteeteae egteetgeae eaggactgge tgaatggeaa ggagtacaag 1020 tgeaaggtet ecaacaaage eeteecagee eecategaga aaaceatete eaaagecaaa 1080 gggeageeee gagaaceae ggtgtacaee etgeeceeat eegggatga getgaceaag 1140 aaceaggtea geetgacetg eetggteaaa ggettetate eeagegacat egeegtggag 1200 tgggagagea atgggeagee ggagaacaae tacaagacea egeeteeegt getggactee 1260 gaeggeteet tetteeteta eageaagete accgtggaca agageaggtg geageagggg 1320 aacgtettet eatgeteegt gatgeatgag getetgeaea accaetaeae geagaagage 1380 eteteeetgt eteegggtaa atga

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<211>467
<212> PRT
<213> Artificial Sequence
<223> Chimeric Sequence
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Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
                   25
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
    35
                 40
                              45
Thr Ala Tyr Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
               55
                           60
Glu Trp Met Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn
                         75
Glu Lys Phe Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
                      90
         85
                                  95
Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
                                 110
Tyr Tyr Cys Ala Arg Ser Gly Asp Gly Ser Arg Phe Val Tyr Trp Gly
                  120
                               125
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
  130
               135
                             140
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
             150
                          155
                                        160
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                      170
                                    175
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                                 190
       180
                    185
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
    195
                  200
                               205
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
               215
                             220
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
225
             230
                          235
                                        240
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                      250
                                    255
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
       260
                    265
                                 270
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Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
                  280
                               285
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
  290
               295
                            300
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
             310
                          315
                                        320
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                      330
                                   335
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                    345
                                 350
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
                  360
                               365
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
  370
               375
                            380
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385
             390
                          395
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                      410
                                   415
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                    425
                                 430
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
                  440
    435
                               445
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
  450
               455
Pro Gly Lys
465
<210> 32
<211>448
<212> PRT
<213> Artificial Sequence
<220>
<223> Chimeric Sequence
<400> 32
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1
                      10
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ala Tyr
                   25
Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
                 40
                              45
Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn Glu Lys Phe
               55
                           60
Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
                         75
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                      90
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Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
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Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
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gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg 432 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala 130 135 140

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Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

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Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met 245 250 255

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gtg gtg agc cac 816

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

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tta gcc tgg tac cag cag aag cca ggt aag gct cca aag ctg ctg atc 144 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile 35 40 45
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ttc ggc caa ggg acc aag gtg gaa atc aaa cga act gtg gct gca cca 336 Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro 100 105 110
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agt gte aca gag cag gac age aag gac age ace tac age etc age age 528 Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser 165 170 175

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Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
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Leu Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
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Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
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Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
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Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
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Thr Thr Ile Phe Gly Val Leu Ile Ile Thr Gly Met Asp Tyr Trp Gly
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